

Table 5: Genes induced in Mycobacterium tuberculosis ideR complemented mutant compared to H37Rv The following microarray data are for individual interpretation. All genes in this table may not be reproducibly induced. In addition, the table should not be seen as a complete list of all possibly induced genes. Description of the data table details and analysis methods are described in the data analysis section.

Spot	Name	Gene	Corrected intensity Average		Average Corrected ratios			Gene product	PCR F	Individual array ratios (CH2/CH1)					
			CH1	CH2	CH2/CH1	StD	SEM			Biol. set 1		Biol. set 2		Biol. set 3	
			Cye3	Cye5	Induced					mm708	mm715	mm698	mm711	mm713	mm621
1493	Rv0011c	-	654	1051	1.6	0.2	0.1		1.1	1.4	1.8	1.4	1.8	1.8	1.5
2767	Rv0116c	-	1506	4082	2.7	0.6	0.2		1.2	3.1	2.7	2.1	3.6	2.6	2.2
5587	Rv0145	-	1213	2368	1.9	0.5	0.2		1.1	2.0	2.0	2.2	2.2	2.2	0.9
4358	Rv0164	-	887	1301	1.5	0.2	0.1		1.1	1.6	1.8	1.3	1.4	1.5	1.4
243	Rv0202c	mmpL11	738	1355	1.6	0.4	0.2	conserved_large_membrane_protein	1.1	1.2	1.5	2.4	1.6	1.5	1.3
2335	Rv0211	pckA	866	1952	2.3	0.4	0.1	phosphoenolpyruvate_carboxykinase_	1.1	2.8	2.4	2.0	2.0	2.6	1.9
1614	Rv0212c	nadR	276	420	1.5	0.4	0.2	similar_to_E.coli_NadR	1.1	1.0	1.4	1.7	2.0	1.2	1.8
170	Rv0267	narU	422	724	1.7	0.2	0.1	similar_to_nitrite_extrusion_protein_2	1.1	1.9	1.9	1.4	1.8	1.9	1.5
3135	Rv0277c	-	695	1058	1.5	0.1	0.1		1.1	1.4	1.3	1.5	1.5	1.7	1.6
1968	Rv0324	-	222	282	1.6	0.3	0.2	putative_transcriptional_regulator	1.1	nd	nd	1.5	1.9	nd	1.3
2694	Rv0333	-	1205	2700	2.2	0.2	0.1		1.1	2.4	2.5	2.0	2.3	2.2	2.1
3896	Rv0422c	thiD	422	774	1.8	0.4	0.2	phosphomethylpyrimidine_kinase	1.1	2.4	1.7	1.3	2.1	1.8	1.3
4212	Rv0467	aceA	565	1002	1.8	0.2	0.1	isocitrate_lyase	1.1	1.9	1.6	1.8	2.0	1.6	1.7
4628	Rv0549c	-	405	1056	1.7	1.5	0.8		1.1	1.1	1.0	nd	4.0	0.7	nd
4632	Rv0557	-	315	463	1.5	0.1	0.1	S76126	1.1	1.4	1.5	1.4	1.6	1.3	1.7
452	Rv0587	-	855	2148	2.5	0.3	0.1	part_of_mce2_operon	1.1	2.8	2.5	2.2	2.9	2.5	2.2
450	Rv0603	-	432	773	1.8	0.1	0.1		2.1	2.0	1.8	1.7	1.7	1.8	1.6
616	Rv0682	rpsL	1802	2839	1.5	0.3	0.1	30S_ribosomal_protein_S12	1.1	nd	1.8	1.3	1.6	1.8	1.2
5498	Rv0712	-	544	939	1.7	1.3	0.6		1.1	1.0	1.2	1.1	4.1	nd	1.1
1890	Rv0715	rplX	740	1445	2.0	0.3	0.1	50S_ribosomal_protein_L24	1.1	2.4	2.3	1.6	2.0	2.1	1.7
5300	Rv0839	-	363	541	1.5	0.1	0.1		1.1	1.5	1.5	1.4	1.5	1.3	1.7
140	Rv0878c	PPE	375	603	1.6	0.2	0.1		1.1	1.4	1.7	1.7	1.7	1.8	1.3
3750	Rv0891c	-	562	878	1.6	0.1	0.1	putative_transcriptional_regulator	1.1	1.7	1.4	1.6	1.6	1.4	1.6
2460	Rv0930	pstA1	791	1194	1.5	0.1	0.1	PstA_component_of_phosphate_uptake	1.1	1.6	1.4	1.6	1.6	1.4	1.3
4027	Rv0948c	-	706	1128	1.6	0.2	0.1		1.1	1.8	1.6	1.5	1.6	1.4	1.4
2191	Rv1006	-	547	830	1.5	0.1	0.0		1.1	1.7	1.6	1.4	1.5	1.6	1.4
267	Rv1010	ksgA	326	461	1.5	0.1	0.1	16S_rRNA_dimethyltransferase	1.1	nd	1.7	1.6	1.5	1.4	1.3
4554	Rv1073	-	868	1283	1.5	0.1	0.0		1.1	1.6	1.5	1.4	1.5	1.4	1.7
1669	Rv1080c	greA	1038	1675	1.6	0.1	0.0	transcription_elongation_factor_G	2.5	1.6	1.8	1.6	1.6	1.6	1.6
563	Rv1168c	PPE	375	665	1.8	0.2	0.1		1.1	1.9	2.0	1.7	1.6	1.8	1.8
1285	Rv1169c	PE	386	712	1.9	0.4	0.2		1.1	2.5	2.1	1.5	1.6	1.8	1.7

4302	Rv1171	-	415	595	1.5	0.1	0.0	hydrophobic_protein	1.1	1.6	1.5	1.3	1.4	1.6	1.4
3452	Rv1182	papA3	2110	3209	1.5	0.3	0.1	PKS-associated_protein_unknown_function	1.1	2.0	1.6	1.3	1.5	1.6	1.3
4174	Rv1183	mmpL10	1055	1758	1.7	0.2	0.1	conserved_large_membrane_protein	1.1	1.8	1.7	1.6	1.6	1.9	1.5
3453	Rv1184c	-	2264	4124	1.9	0.2	0.1		1.1	1.9	2.0	1.7	1.7	2.2	1.7
1481	Rv1195	PE	367	1111	3.0	0.4	0.2		1.1	2.7	2.9	3.2	3.3	3.5	2.4
2203	Rv1196	PPE	1638	2717	1.6	0.2	0.1		1.1	2.0	1.6	1.7	1.7	1.6	1.2
1482	Rv1197	-	4447	6669	1.5	0.2	0.1		1.1	1.7	1.6	1.3	1.4	1.8	1.2
1483	Rv1199c	IS1081	968	1578	1.6	0.2	0.1		1.1	1.4	1.5	1.8	1.8	1.6	1.3
771	Rv1347c	-	218	366	1.7	0.2	0.1	possible_aminoglycoside_6'-N-acetyltransferase	1.1	1.7	1.8	1.4	1.9	1.7	1.7
3157	Rv1357c	-	314	473	1.5	0.3	0.1		1.1	1.0	1.3	1.8	1.7	1.5	1.5
3660	Rv1361c	PPE	1442	3059	2.1	0.3	0.1		1.4	2.3	2.2	2.2	2.2	2.1	1.6
137	Rv1373	-	300	455	1.5	0.2	0.1	slight_similarity_to_sulfotransferases	1.1	1.1	1.7	1.6	1.7	1.5	1.4
138	Rv1375	-	349	531	1.5	0.1	0.1		1.1	1.5	1.7	1.6	1.5	1.3	1.5
1897	Rv1397c	-	614	914	1.5	0.1	0.0		1.1	1.6	1.5	1.4	1.5	1.5	1.5
2619	Rv1398c	-	4471	7494	1.7	0.2	0.1		1.1	2.1	1.7	1.5	1.6	1.7	1.4
4788	Rv1414	-	235	396	1.7	0.2	0.1		1.1	1.6	1.5	2.0	1.4	1.5	1.9
5510	Rv1415	ribA2	1257	2563	2.0	0.3	0.1	probable_GTP_cyclohydrolase_II	1.1	2.2	2.1	1.7	2.4	1.8	2.0
4809	Rv1504c	-	530	907	1.7	0.3	0.1		1.1	1.3	nd	2.1	2.0	1.4	1.7
2952	Rv1639c	-	1388	2055	1.5	0.1	0.0		1.1	1.5	1.7	1.4	1.4	1.5	1.5
3279	Rv1738	-	2981	4971	1.8	0.7	0.3		1.1	2.7	2.2	0.9	1.1	1.9	1.9
3741	Rv1769	-	983	1776	1.5	0.9	0.3		1.1	3.1	1.2	0.7	1.6	1.5	0.7
4467	Rv1854c	ndh	1052	1607	1.5	0.2	0.1	probable_NADH_dehydrogenase	1.4	1.3	1.4	1.9	1.6	1.4	1.3
3221	Rv1870c	-	601	1469	2.5	0.2	0.1		1.1	2.9	2.4	2.5	2.4	2.3	2.3
2983	Rv1872c	lldD2	2177	3102	1.5	0.2	0.1	L-lactate_dehydrogenase	1.1	1.6	1.6	1.2	1.3	1.5	1.7
2974	Rv1902c	nanT	528	796	1.5	0.1	0.1	probable_sialic_acid_transporter_	1.1	1.5	1.4	1.4	1.6	1.7	1.4
2973	Rv1904	-	493	807	1.6	0.1	0.1		1.1	1.4	1.6	1.6	1.7	1.7	1.8
812	Rv1905c	aaO	416	618	1.5	0.1	0.0	D-amino_acid_oxidase	1.1	1.5	1.4	1.6	1.5	1.4	1.4
85	Rv1917c	PPE	678	1022	1.5	0.3	0.1		1.4	1.3	1.4	1.8	1.6	1.6	1.1
5556	Rv1979c	-	969	1744	1.8	0.2	0.1	unknown_permease	1.1	2.0	1.9	1.6	1.9	1.7	1.7
4834	Rv1980c	mpt64	2792	5028	1.8	0.3	0.1	secreted_immunogenic_protein_Mpb64/Mpt64	1.1	2.1	1.9	1.4	1.8	2.2	1.5
1944	Rv1996	-	870	1327	1.6	0.4	0.2		1.2	2.0	2.1	1.1	1.2	1.7	1.6
1681	Rv2031c	hspX	1307	1644	1.5	0.6	0.3	14kD_antigen_heat_shock_protein_Hsp20_family	1.1	1.9	2.3	0.7	0.8	1.6	1.7
1684	Rv2037c	-	478	1236	2.6	0.7	0.3	probable_transmembrane_protein	1.1	3.2	2.6	2.4	3.1	2.6	1.4
4567	Rv2039c	-	667	1540	2.3	0.2	0.1	probable_sugar_transporter	1.1	2.4	2.3	2.1	2.7	2.1	2.2
5211	Rv2098c	PE_PGRS	256	362	1.5	1.4	0.6		2.6	3.9	0.8	nd	0.9	0.8	0.8
4436	Rv2107	PE	236	377	1.6	0.4	0.2		1.1	1.3	1.0	2.0	2.0	1.5	1.5
1553	Rv2117	-	259	381	1.6	0.9	0.4		1.1	nd	2.9	1.1	nd	1.0	1.2

1556	Rv2123	PPE	230	307	1.5	0.4	0.2		1.1	nd	1.2	1.7	nd	1.1	1.8
4442	Rv2128	-	675	1042	1.6	0.1	0.1	unknown_hydrophobic_protein	1.1	1.7	1.7	1.3	1.5	1.6	1.5
3705	Rv2190c	-	1240	2402	1.9	0.3	0.1	putative_p60_homologue	1.1	2.4	2.1	1.7	1.7	1.7	1.9
229	Rv2247	accD6	617	915	1.5	1.3	0.5	acetyl/propionyl_CoA_carboxylase_b_subunit	1.1	4.2	1.1	0.8	0.9	0.8	1.0
3383	Rv2305	-	792	1463	1.5	1.0	0.4		1.1	3.5	1.1	1.0	1.1	1.0	1.1
4509	Rv2336	-	569	865	1.5	0.1	0.1		1.1	1.5	1.7	1.3	1.6	1.6	1.5
1561	Rv2364c	bex	247	374	1.6	0.1	0.0	GTP-binding_protein_of_Era/ThdF_family	1.1	nd	1.5	1.7	1.7	1.5	1.6
1560	Rv2366c	-	307	458	1.5	0.2	0.1		1.1	1.0	1.7	1.5	1.7	1.5	1.5
2281	Rv2367c	-	590	867	1.5	0.2	0.1		1.1	1.4	nd	1.3	1.8	1.5	1.4
471	Rv2380c	mbtE	221	318	1.5	0.2	0.1	mycobactin/exochelin_synthesis_(lysine_ligation)	1.1	1.8	1.6	nd	1.3	1.4	1.5
1192	Rv2381c	mbtD	289	513	1.8	0.1	0.1	mycobactin/exochelin_synthesis_(polyketide_synthase)	1.1	2.0	1.6	1.7	1.7	1.9	1.7
2273	Rv2386c	trpE2	254	492	1.9	0.2	0.1	anthranilate_synthase_component_I	1.1	2.2	2.0	1.7	1.9	1.8	2.0
2270	Rv2392	cysH	1212	1811	1.5	0.2	0.1	3'-phosphoadenylylsulfate_(PAPS)_reductase	1.1	1.6	1.4	1.2	1.7	1.5	1.5
1544	Rv2412	rpsT	485	710	1.5	0.2	0.1	30S_ribosomal_protein_S20	1.1	1.3	1.8	1.2	1.6	1.8	1.4
3654	Rv2428	ahpC	1042	2427	2.4	0.8	0.3	alkyl_hydroperoxide_reductase	1.1	2.6	1.8	1.9	2.6	3.7	1.6
2932	Rv2429	ahpD	396	802	2.1	0.4	0.2	member_of_AhpC/TSA_family	1.1	1.9	2.0	nd	2.3	2.6	1.7
4122	Rv2430c	PPE	1025	1724	1.7	0.2	0.1		1.1	2.0	1.6	1.6	1.6	1.9	1.4
3400	Rv2431c	PE	407	650	1.6	0.1	0.1		1.1	1.8	1.4	1.6	1.5	1.6	1.6
5247	Rv2452c	-	345	557	1.6	0.1	0.1		1.1	1.7	1.6	1.4	1.8	1.6	1.4
4529	Rv2459	-	964	1891	1.7	0.6	0.3	probable_drug_efflux_protein	1.1	1.5	1.8	1.3	2.9	1.2	1.4
415	Rv2512c	IS1081	473	733	1.5	0.2	0.1		1.1	1.6	1.4	1.7	1.8	1.7	1.2
1653	Rv2516c	-	377	593	1.6	0.2	0.1		1.1	1.3	1.5	1.6	1.7	1.5	1.8
4868	Rv2564	glnQ	296	469	1.6	0.3	0.1	probable_ATP-binding_transport_protein	1.1	1.3	1.3	1.9	1.9	nd	1.6
2992	Rv2590	fadD9	560	917	1.7	0.1	0.1	acyl-CoA_synthase	1.1	1.6	1.7	1.5	1.8	1.7	nd
457	Rv2623	-	291	454	1.6	0.4	0.2		1.1	1.9	2.2	1.2	1.1	1.6	1.7
456	Rv2625c	-	395	592	1.5	0.2	0.1		1.1	1.6	1.7	1.3	1.3	1.6	1.6
1177	Rv2626c	-	555	991	1.9	0.7	0.3		1.1	3.0	2.2	1.0	1.1	2.0	1.9
454	Rv2629	-	475	734	1.6	0.3	0.1		1.1	1.9	1.9	1.2	1.2	1.5	1.6
518	Rv2632c	-	1242	1892	1.5	0.3	0.1		1.1	1.9	1.8	1.2	1.4	1.8	1.3
55	Rv2683	-	305	456	1.6	0.3	0.1		1.1	2.0	1.5	1.4	1.4	1.5	nd
56	Rv2685	arsB	286	422	1.5	0.1	0.0	probable_arsenical_pump	1.1	1.3	1.7	1.5	1.4	1.5	1.5
2934	Rv2710	sigB	1229	1860	1.5	0.4	0.1	RNA_polymerase_sigma_factor_(aka_MysB)	1.1	1.3	1.4	1.7	1.7	2.0	1.0
3653	Rv2711	ideR	785	2407	3.1	0.8	0.4	iron_dependent_repressor_ideR	1.1	3.4	nd	2.7	3.8	3.8	2.0
3882	Rv2712c	-	407	891	2.2	0.4	0.2		1.1	2.0	1.8	2.6	2.9	2.2	1.9
2491	Rv2724c	fadE20	577	859	1.5	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	1.2	1.2	2.0	1.8	1.3	1.2
2969	Rv2800	-	367	1009	3.1	1.2	0.6		1.1	1.5	3.6	nd	3.3	4.3	nd
79	Rv2816c	-	1129	1739	1.5	0.3	0.1		1.1	1.7	1.8	1.2	1.5	1.8	1.2

3688	Rv2817c	-	1101	1739	1.6	0.2	0.1		1.1	2.0	1.4	1.6	1.4	1.5	1.4
1217	Rv2919c	glnB	604	900	1.5	0.2	0.1	nitrogen_regulatory_protein	1.1	1.5	1.4	1.7	1.5	1.5	1.2
755	Rv2930	fadD26	720	1464	2.0	0.3	0.1	acyl-CoA_synthase	1.1	2.4	2.0	1.8	2.2	2.2	1.6
34	Rv2931	ppsA	355	590	1.6	0.2	0.1	phenolphthiocerol_synthase_(pksB)	1.1	1.6	1.6	1.8	1.8	1.7	1.4
4548	Rv3010c	pfkA	534	1067	2.0	0.2	0.1	phosphofructokinase_I	1.1	2.1	2.1	2.0	2.0	1.6	2.3
4891	Rv3033	-	342	533	1.6	0.1	0.0		1.1	1.7	1.6	1.5	1.6	1.5	1.5
2593	Rv3095	-	1066	2622	2.8	1.0	0.6	putative_transcriptional_regulator	1.1	3.2	nd	nd	3.7	nd	1.7
5484	Rv3126c	-	886	1428	1.7	0.4	0.2		1.1	2.1	2.2	1.2	1.3	1.7	1.8
4763	Rv3127	-	973	1517	1.7	0.5	0.2		1.1	2.1	2.2	1.2	1.0	1.6	1.8
4764	Rv3128c	-	250	381	1.6	0.2	0.1		1.1	1.5	1.8	1.5	1.3	1.5	1.8
3036	Rv3130c	-	725	1212	1.7	0.3	0.1		2.6	1.9	2.1	1.4	1.4	2.0	1.7
227	Rv3140	fadE23	697	1486	2.2	0.3	0.1	acyl-CoA_dehydrogenase_	1.1	2.3	2.1	1.7	2.5	2.1	2.3
1305	Rv3170	-	582	1093	1.6	0.6	0.3	Probable_flavin-containing_monoamine_oxidase	1.1	1.2	1.0	2.4	1.3	1.3	2.5
4191	Rv3178	-	983	2824	2.9	0.7	0.3		1.1	3.7	2.6	2.2	3.6	2.4	nd
3541	Rv3229c	desA3	1129	3756	3.6	2.0	0.8	acyl-[ACP]_desaturase	1.1	2.4	2.2	5.6	6.7	2.9	1.9
4263	Rv3230c	-	1157	1865	1.6	0.3	0.1	similar_to_various_oxygenases	1.1	1.5	1.6	1.7	2.1	1.6	1.2
3068	Rv3269	-	448	711	1.7	0.3	0.1	probable_heat_shock_protein	1.1	1.7	2.2	1.2	1.4	1.8	1.8
906	Rv3278c	-	562	893	1.6	0.2	0.1		1.1	1.6	1.8	1.5	1.7	nd	1.3
537	Rv3402c	-	320	497	1.5	0.2	0.1	possible_involved_in_LPS_synthase	1.1	1.3	1.6	1.8	1.6	1.4	1.5
293	Rv3454	-	313	463	1.5	0.3	0.1	some_similarity_to_proline_permeases	1.3	1.0	1.7	1.6	1.6	1.2	1.6
1021	Rv3479	-	1319	2058	1.6	0.3	0.1		1.1	2.0	1.7	1.4	1.3	1.6	1.5
3906	Rv3485c	-	396	587	1.5	0.2	0.1	short-chain_alcohol_dehydrogenase_family	1.1	1.4	1.2	1.7	1.6	1.3	1.6
3185	Rv3486	-	745	1274	1.7	0.1	0.0		1.1	1.7	1.5	1.8	1.8	1.7	1.7
3186	Rv3487c	lipF	778	1183	1.5	0.2	0.1	probable_esterase	1.1	1.7	1.5	1.4	1.4	1.5	1.7
3785	Rv3583c	-	3593	5352	1.5	0.3	0.1	putative_transcriptional_regulator	1.1	1.9	1.7	1.3	1.3	nd	1.2
3533	Rv3588c	-	688	1253	1.8	0.2	0.1	putative_carbonic_anhydrase	1.1	2.2	2.0	1.6	1.8	1.8	1.7
278	Rv3611	-	453	782	1.7	0.2	0.1		2.6	1.4	1.9	1.7	1.6	1.7	1.9
1270	Rv3612c	-	1055	1586	1.5	0.3	0.1		1.1	2.0	1.4	1.3	1.3	1.7	1.5
548	Rv3613c	-	1352	2405	1.8	0.2	0.1		1.1	2.0	1.9	1.8	1.6	1.8	1.6
4157	Rv3614c	-	3437	5789	1.7	0.3	0.1		1.1	2.1	2.0	1.3	1.3	1.8	1.6
309	Rv3623	lpqG	297	419	1.5	0.1	0.0		1.1	nd	1.5	1.4	1.7	1.4	1.4
306	Rv3641c	fic	258	388	1.5	0.2	0.1	possible_cell_division_protein	1.1	1.1	1.7	1.6	1.5	1.4	1.6
5011	Rv3662c	-	890	1581	1.5	0.2	0.1		1.1	nd	1.8	1.4	1.5	1.3	1.6
4601	Rv3679	-	1167	1750	1.5	0.3	0.1	possible_anion_transporter	1.1	1.8	1.9	1.3	nd	1.3	1.5
1718	Rv3689	-	1524	2281	1.5	0.1	0.0	hydrophobic_highly_Proline_rich_N-terminus	2.5	1.4	1.6	1.5	1.5	1.6	1.4
223	Rv3804c	fbpA	1427	2107	1.5	0.2	0.1	antigen_85A_mycolyltransferase	1.1	1.8	1.6	1.2	1.5	1.7	1.3



